Reviewer Report

Title: Genomic diversity affects the accuracy of bacterial SNP calling pipelines

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Reviewer name: C. Titus Brown

Reviewer Comments to Author:

In this paper, Bush et al. evaluate a large number of bacterial SNP
calling pipelines against variously divergent references. Their main
conclusion is that different pipelines perform very differently
as the reference diverges, and that Jaccard similarity is a good way to
choose the "best" (closest) reference for mapping.
This paper is full of nice figures and analyses, and moreover we have
seen the same thing in our work, so I agreed with the major points of
the paper in advance!
The only real weakness I see in the paper is that the authors use simulated
data, which comes with many advantages but also means that oddball sequencer
mistakes are not necessarily measured. This is an acceptable tradeoff to me,
but I wanted to mention it...
I think the general conclusion that Jaccard similarity (or, really, ANI)
is the best way to choose reference genomes is both important and
indisputable, so it's nice to see a thorough evaluation of it.
I encourage the authors to make their evaluation code, scripts,
notebooks, figure generation, etc. available. I could not seem to find
it. Reproducibility is minimal but acceptable given Supp Text 1.

Methods

Are the methods appropriate to the aims of the study, are they well described, and are necessary
controls included? Choose an item.

Conclusions

Are the conclusions adequately supported by the data shown? Choose an item.

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